



results of **BLAST**

BLASTP 2.2.7 [Dec 30 2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1072811300-17465-209900690670.BLASTQ4

Query=

(471 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

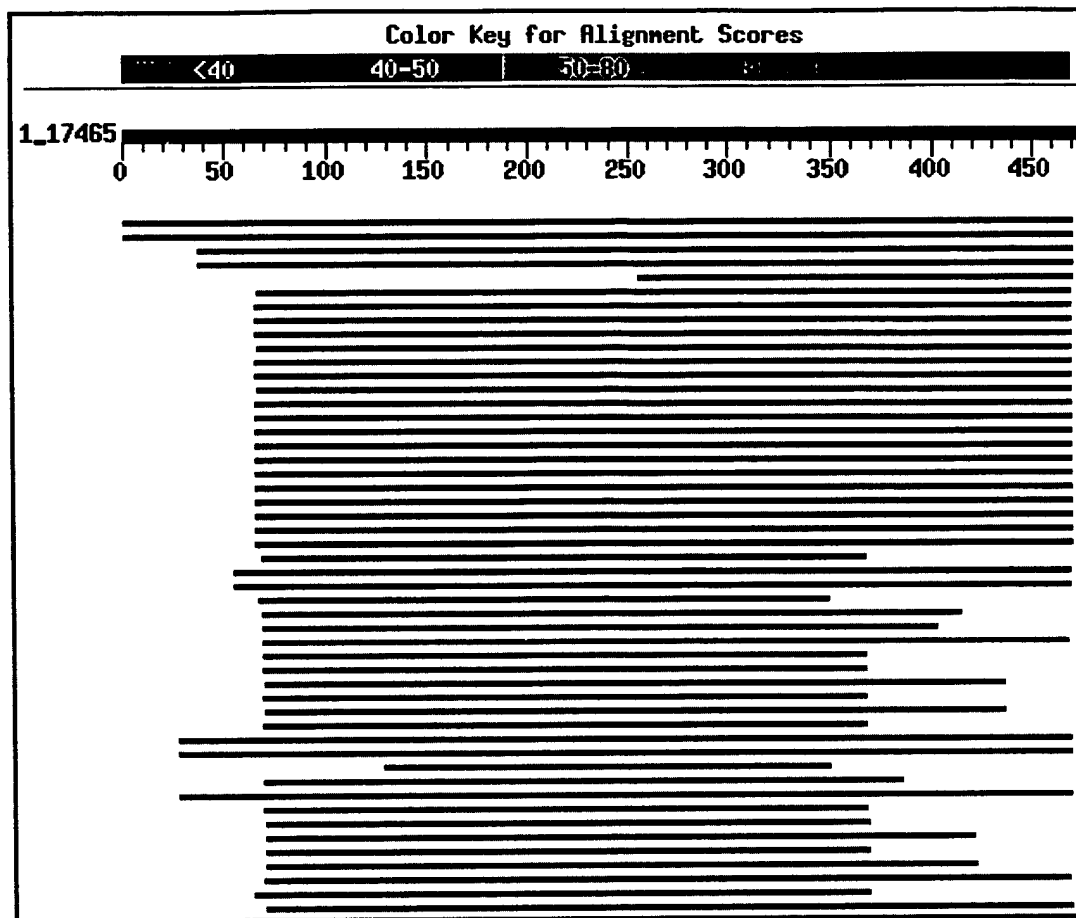
1,585,607 sequences; 519,349,222 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 50 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score	E
(bits)	Value

gi 32699007 ref NP_872395.1 	5-hydroxytryptamine serotonin ...	954	0.0	L
gi 37574914 qb AAQ93477.1 	5-HT3cl serotonin receptor-like ...	924	0.0	L
gi 38146010 ref NP_938055.1 	5-hydroxytryptamine serotonin ...	854	0.0	L
gi 18640740 ref NP_570126.1 	5-hydroxytryptamine receptor 3...	681	0.0	L
gi 32698904 ref NP_872343.1 	5-hydroxytryptamine receptor 3...	367	e-100	L
gi 9790622 qb AAB37533.2 	5-hydroxytryptamine type 3AS rece...	291	2e-77	L
gi 30583247 qb AAP35868.1 	5-hydroxytryptamine (serotonin) ...	291	3e-77	L
gi 4504543 ref NP_000860.1 	5-hydroxytryptamine (serotonin)...	291	3e-77	L
gi 30585371 qb AAP36958.1 	Homo sapiens 5-hydroxytryptamine...	291	3e-77	
gi 1586341 prf 2203408A	serotonin 3AS receptor	290	5e-77	
gi 2978508 qb AAC06137.1 	5-HT3-As receptor precursor [Cavi...	287	3e-76	
gi 13242306 ref NP_077370.1 	5-hydroxytryptamine (serotonin...	285	9e-76	L
gi 8247752 dbj BAA96417.1 	ferret 5-HT3A receptor [Mustela ...	285	1e-75	
gi 1168223 sp P35563 5HT3_RAT	5-hydroxytryptamine 3 recepto...	284	2e-75	L
gi 2144046 pir I58179	5HT3 receptor subunit - rat (fragmen...	283	4e-75	
gi 488695 emb CAA55871.1 	5HT3 receptor [Mus musculus]	283	5e-75	L
gi 24211440 sp O70212 5HT3_CAVPO	5-hydroxytryptamine 3 rece...	283	7e-75	
gi 7305175 ref NP_038589.1 	5-hydroxytryptamine (serotonin)...	282	1e-74	L
gi 543183 pir S41757	5-hydroxytryptamine-3 receptor - mouse	281	2e-74	

gi 488694 emb CAA55870.1	5HT3 receptor [Mus musculus]	281	2e-74	L
gi 21314591 gb AAM47014.1	5-hydroxytryptamine receptor 3A ...	281	2e-74	L
gi 313864 emb CAA51089.1	5-hydroxytryptamine3 receptor [Mu...	280	3e-74	L
gi 817940 emb CAA80453.1	5HT3 receptor [Mus musculus]	279	7e-74	L
gi 3115222 emb CAA05851.1	serotonin receptor [Homo sapiens]	274	3e-72	L
gi 28277272 gb AAH44101.1	MGC52789 protein [Xenopus laevis]	213	5e-54	L
gi 9938026 ref NP_064670.1	5-hydroxytryptamine (serotonin)...	213	8e-54	L
gi 11559956 ref NP_071525.1	5-hydroxytryptamine (serotonin)...	212	1e-53	L
gi 5174469 ref NP_006019.1	5-hydroxytryptamine (serotonin)...	206	8e-52	L
gi 31790123 gb AAP58387.1	nicotinic acetylcholine receptor...	176	6e-43	
gi 31790121 gb AAP58386.1	nicotinic acetylcholine receptor...	173	6e-42	
gi 7407125 gb AAF61920.1	nicotinic acetylcholine receptor ...	171	3e-41	L
gi 9501306 emb CAB99482.1	alpha 10 subunit of nicotinic ac...	171	3e-41	
gi 8923742 ref NP_060051.1	cholinergic receptor, nicotinic...	171	4e-41	L
gi 5777609 emb CAB53472.1	nicotinic acetylcholine receptor...	170	4e-41	L
gi 38081753 ref XP_132045.2	cholinergic receptor, nicotini...	170	6e-41	L
gi 31542395 ref NP_067344.2	cholinergic receptor, nicotini...	170	7e-41	L
gi 31790117 gb AAP58384.1	nicotinic acetylcholine receptor...	169	1e-40	
gi 27532980 ref NP_775304.1	cholinergic receptor, nicotini...	168	2e-40	L
gi 18542399 gb AAL75573.1	nicotinic acetylcholine receptor...	168	2e-40	L
gi 11120504 gb AAG30903.1	5-hydroxytryptamine 3 receptor B...	168	2e-40	L
gi 6692362 gb AAF24618.1	neuronal acetylcholine receptor s...	167	4e-40	
gi 19424304 ref NP_598281.1	cholinergic receptor, nicotini...	167	6e-40	L
gi 12621088 ref NP_075219.1	acetylcholine receptor alpha 9...	166	9e-40	L
gi 31745832 gb AAP57217.1	nicotinic acetylcholine receptor...	166	1e-39	
gi 17105332 ref NP_476532.1	cholinergic receptor, nicotini...	165	2e-39	L
gi 34878975 ref XP_346491.1	hypothetical protein XP_346490...	164	3e-39	L
gi 34148146 gb AAQ62631.1	nicotinic acetylcholine receptor...	164	3e-39	
gi 11138123 ref NP_065135.2	cholinergic receptor, nicotini...	163	5e-39	L
gi 31745830 gb AAP57216.1	nicotinic acetylcholine receptor...	162	9e-39	
gi 104800 pir B39218	nicotinic acetylcholine receptor alph...	162	9e-39	

Alignments

Get selected sequences Select all Deselect all

>gi|32699007|ref|NP_872395.1| L 5-hydroxytryptamine serotonin receptor 3E [Homo
gi|31790914|gb|AAO38167.1| L 5-hydroxytryptamine serotonin receptor 3E [Homo sapi
Length = 471

Score = 954 bits (2467), Expect = 0.0

Identities = 467/471 (99%), Positives = 469/471 (99%)

Query: 1 MLAFILSRATPRPALGPLSYREHRVALLHLTHSMSTTGRGVFTFTINCSGFGQHGDPTAV 60
MLAFILSRATPRPALGPLSYRE RVALLHLTHSMSTTGRGVFTFTINCSGFGQHGDPTA+
Sbjct: 1 MLAFILSRATPRPALGPLSYRERRVALLHLTHSMSTTGRGVFTFTINCSGFGQHGDPTAL 60

Query: 61 NSVFNRKPFPRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPE 120
NSVFNRKPFPRPVTNISV TQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPE

Sbjct: 61 NSVFNRKPFPRPVTNISVLTVQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPE 120

Query: 121 ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD 180
ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD

Sbjct: 121 ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD 180

Query: 181 IFYFPFDQQNCTLTFFSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA 240
IFYFPFDQQNCTLTFFSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA

Sbjct: 181 IFYFPFDQQNCTLTFFSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA 240

Query: 241 KLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL 300
KLSRGGNLYD+IVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL

Sbjct: 241 KLSRGGNLYDRIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL 300

Query: 301 LLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR 360
LLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR



Sbjct: 301 LLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR 360

Query: 361 WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGGSE 420
WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGGSE

Sbjct: 361 WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGGSE 420

Query: 421 WTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLFMASSIITVICLWNT 471
WTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLFMASSIITVICLWNT

Sbjct: 421 WTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLFMASSIITVICLWNT 471

 >gi|37574914|qb|AAQ93477.1|  5-HT3c1 serotonin receptor-like protein [Homo sapiens]
Length = 456

Score = 924 bits (2387), Expect = 0.0

Identities = 455/471 (96%), Positives = 456/471 (96%), Gaps = 15/471 (3%)

Query: 1 MLAFILSRATPRPALGPLSYREHRVALLHLTHSMSTTGRGVFTFTINCSGFGQHGDPTAV 60
MLAFILSRATPRPALGPLSYREHRVALLHLTHSMSTTGRGVFTFTINCSGFGQHGDPTA+

Sbjct: 1 MLAFILSRATPRPALGPLSYREHRVALLHLTHSMSTTGRGVFTFTINCSGFGQHGDPTAL 60

Query: 61 NSVFNRKPFPRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPE 120
NSVFNRKPFPRPVTNISVPTQVNISFAMSAILDV VWDNPFISWNPE

Sbjct: 61 NSVFNRKPFPRPVTNISVPTQVNISFAMSAILDV-----VWDNPFISWNPE 105

Query: 121 ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD 180
ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD

Sbjct: 106 ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD 165

Query: 181 IFYFPFDQQNCTLTFFSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA 240
IFYFPFDQQNCTLTFFSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA

Sbjct: 166 IFYFPFDQQNCTLTFFSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA 225

Query: 241 KLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL 300
KLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL

Sbjct: 226 KLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL 285

Query: 301 LLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR 360
LLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR

Sbjct: 286 LLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR 345




Query: 361 WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGGSE 420
WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGGSE

Sbjct: 346 WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAAEALTGGSE 405

Query: 421 WTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLFMASSIITVICLWNT 471

WTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLFMASSIITVICLWNT

Sbjct: 406 WTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLFMASSIITVICLWNT 456

 >gi|38146010|ref|NP_938055.1|  5-hydroxytryptamine serotonin receptor 3E [Homo
gi|37574912|gb|AAQ93476.1|  5-HT3c1 serotonin receptor-like protein [Homo sapien
Length = 441

Score = 854 bits (2206), Expect = 0.0

Identities = 418/434 (96%), Positives = 419/434 (96%), Gaps = 15/434 (3%)

Query: 38 GRGVTFTINCSGFGQHGDPTAVNSVFNRKPFPRVTNISVPTQVNISFAMSAILDVNEQL 97

GRGVTFTINCSGFGQHGDPTA+NSVFNRKPFPRVTNISVPTQVNISFAMSAILDV

Sbjct: 23 GRGVTFTINCSGFGQHGDPTALNSVFNRKPFPRVTNISVPTQVNISFAMSAILDV---- 78

Query: 98 HLLSSFLWLEMVWDNPFISWNPEECEGITKMSMAAKNLWLPDIFIIEIEMDVKTPKGLTA 157

VWDNPFISWNPEECEGITKMSMAAKNLWLPDIFIIEIEMDVKTPKGLTA

Sbjct: 79 -----VWDNPFISWNPEECEGITKMSMAAKNLWLPDIFIIEIEMDVKTPKGLTA 127

Query: 158 YVSNEGRIRYKKPMKVDSICNLDFYFPFDQQNCTLTFSFLYTVDMSLLDMEKEVWEIT 217

YVSNEGRIRYKKPMKVDSICNLDFYFPFDQQNCTLTFSFLYTVDMSLLDMEKEVWEIT

Sbjct: 128 YVSNEGRIRYKKPMKVDSICNLDFYFPFDQQNCTLTFSFLYTVDMSLLDMEKEVWEIT 187

Query: 218 DASRNILQTHGEWELLGLSKATAKLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLV 277

DASRNILQTHGEWELLGLSKATAKLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLV

Sbjct: 188 DASRNILQTHGEWELLGLSKATAKLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLV 247

Query: 278 AIDALSFYLPVKSGNRVPFKITLLLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGS 337

AIDALSFYLPVKSGNRVPFKITLLLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGS

Sbjct: 248 AIDALSFYLPVKSGNRVPFKITLLLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGS 307

Query: 338 LLETIFITHLLHVATTQPPPLPRWLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGV 397

LLETIFITHLLHVATTQPPPLPRWLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGV

Sbjct: 308 LLETIFITHLLHVATTQPPPLPRWLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGV 367

Query: 398 KEPEVSAGQMPGPAAEALTGGSEWTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLF 457




KEPEVSAGQMPGPAAEALTGGSEWTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLF

Sbjct: 368 KEPEVSAGQMPGPAAEALTGGSEWTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLF 427

Query: 458 MASSIITVICLWNT 471

MASSIITVICLWNT

Sbjct: 428 MASSIITVICLWNT 441

 >gi|18640740|ref|NP_570126.1|  5-hydroxytryptamine receptor 3 subunit C [Homo :
gi|18251966|gb|AAL66182.1|  5-hydroxytryptamine receptor 3 subunit C [Homo sapie
Length = 447

Score = 681 bits (1756), Expect = 0.0

Identities = 327/434 (75%), Positives = 368/434 (84%), Gaps = 9/434 (2%)

Query: 38 GRGVTFTINCSGFGQHGDPTAVNSVFNRKPFPRVTNISVPTQVNISFAMSAILDVNEQL 97

GRG FTINCSGF QHG DP +VF+RK FRP TN S+PT+VNISF +SAIL V+ QL

Sbjct: 23 GRGDAFTINCSGFDQHGVDPAVFQAVFDRKAFRPFNTNYSIPTRVNISFTLSAILGVDAQL 82

Query: 98 HLLSSFLWLEMVWDNPFISWNPEECEGITKMSMAAKNLWLPDIFIIEIEMDVKTPKGLTA 157
 LL+SFLW+++VWDNPFII+WNPE+EC GI K+++ A+NLWLPDIFI+E MDVD+TP GLTA
 Sbjct: 83 QLLTSFLWMDLVWDNPFINWNPKCECVGINKLTVLAENLWLPDIFIVESMDVDQTPSGLTA 142

Query: 158 YVSNEGRIRYKKPKMKVDSICNLDFIFFPDQQNCTLTFSFLYTVDSMLLDMEKEVWEIT 217
 Y+S+EGRI+Y KPM+V SIC LDIFIFFPDQQNCT TFSSFLYTVDSMLL M+KEVWEIT
 Sbjct: 143 YISSEGRIKYDKPMRVTSICKLDIFIFFPDQQNCTFTFSFLYTVDSMLLGMDKEVWEIT 202

Query: 218 DASRNILQTHGEWELLGLSKATAKLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLV 277
 D SR ++QT GEWELLG++KAT K+S G NLYDQI+FYVAIRRRPSLY+INLLVPS FLV
 Sbjct: 203 DTSRKVIQTQGEWELLGINKATPKMSMGNNLYDQIMFYVAIRRRPSLYIINLLVPSFLV 262

Query: 278 AIDALSFYLPVKSGNRVPFKITLLLGYNVFLLMMSDLLPTSGTPLIGVYFALCLSLMVGS 337
 AIDALSFYLP +S NR PFKITLLLGYNVFLLM+DLLP SGTPLI VYFALCLSLMV S
 Sbjct: 263 AIDALSFYLPAESENRAFPFKITLLLGYNVFLLMNDLLPASGTPLISVYFALCLSLMVVS 322

Query: 338 LLETIFITHLLHVATTQPPPLPRWLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGV 397
 LLET+FIT+LLHVATTQPPP+PRWLHSLLLHC SPGRCCPTAPQK NKG GLT THLPG
 Sbjct: 323 LLETVFITYLLHVATTQPPMPRWLHSLLLHCTSPGRCCPTAPQKGNKGLGLTLTHLPGP 382

Query: 398 KEPEVSAGQMPGPAEAEELTGGSEWTRAQREHEAQKQHSVELWLQFSHAMDLFRLYLLF 457
 KEP AG+ GP E E GGS WT+ Q +ELW+QFSHAMD +LFRLYLLF
 Sbjct: 383 KEPGELAGKKLGPTEPEDGGSAAWTKTQL-----MELWVQFSHAMDTLLFRLYLLF 433

Query: 458 MASSIITVICLWNT 471
 MASSI+TVI LWNT
 Sbjct: 434 MASSILTVIVLWNT 447

└>gi|32698904|ref|NP_872343.1| **L** 5-hydroxytryptamine receptor 3 subunit D; similar
 5-hydroxytryptamine receptor 3 subunit C [Homo sapiens]
 gi|31790912|gb|AAO38166.1| **L** 5-hydroxytryptamine serotonin receptor 3D [Homo sapiens]
 Length = 279

Score = 367 bits (943), Expect = e-100

Identities = 188/232 (81%), Positives = 200/232 (86%), Gaps = 16/232 (6%)

Query: 256 VAIRRR--PSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLLLGYNVFLLMMSD 313
 VAIR R PS YV+N LVPSG L+AIDALSFYLP +SGN PFK+T+LLGY+VFLLM+D
 Sbjct: 48 VAIRHRCRSPYVNFVFLVPSGILIAIDALSFYLPPESGNCAPFKMTVLLGYSVFLLMND 107

Query: 314 LLPTSGTP----LI-----GVYFALCLSLMVGSLLLETIFITHLLHVATTQPPPLP 359
 LLP + T L+ GVYFALCLSLMVGSLLLETIFITHLLHVATTQPP PLP
 Sbjct: 108 LLPATSTSSHASLVRPHPSRDQKRGVYFALCLSLMVGSLLLETIFITHLLHVATTQPLPLP 167

Query: 360 RWLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGG 419
 RWLHSLLLHC GRCCPTAPQK NKGPG+TPTHLPGVKEPEVSAGQMPGP EAEELTGG
 Sbjct: 168 RWLHSLLLHCTGQGRCCPTAPQKGNKGPVTPPTHLPGVKEPEVSAGQMPGPGEAEELTGG 227

Query: 420 EWTRAQREHEAQKQHSVELWLQFSHAMDLFRLYLLFMASSIITVICLWNT 471
 EWTRAQREHEAQKQHSVELW+QFSHAMDA+LFRLYLLFMASSIITVICLWNT
 Sbjct: 228 EWTRAQREHEAQKQHSVELWVQFSHAMDALLFRLYLLFMASSIITVICLWNT 279

└>gi|9790622|gb|AAB37533.2| **L** 5-hydroxytryptamine type 3AS receptor subunit [Homo sapiens]
 Length = 478

Score = 291 bits (745), Expect = 2e-77

Identities = 170/432 (39%), Positives = 254/432 (58%), Gaps = 33/432 (7%)

Query: 67 KPFRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPEECEGIT 126
 K RPV + PT V+I + AIL+V+E+ +L+++W W + F+ WNPE+ + IT
 Sbjct: 47 KGVPRVDRWRKPTTVSIDVIVYAILNVDEKNQVLTYYIWRQYWTDEFLQWNPEDFDNIT 106

Query: 127 KMSMAAKNLWLPDIFIIEIEMDVKTPKGLTAYVSNEGRIRYKKPMKVDSICNLDIFYFPF 186
 K+S+ ++W+PDI I EL+DV K+P Y+ ++G ++ KP++V + C+LDI+ FPF
 Sbjct: 107 KLSIPTDSIWVPDILINELVDVGKSPNIPYVYIRHQGEVQNYKPLQVVTACSLDIYNFPF 166

Query: 187 DQQNCTLTFSFLYTVDSMLLDMEKEVWEITD---ASRNILQTHGEWELLGLSKATAKLS 243
 D QNC+LTF+S+L+T+ D+ +W + + + R++ GEWELLG+ + S
 Sbjct: 167 DVQNCSLTFTSWLHTIQ----DINISLWRLPEKVKSDRSVFMNQGEWELLGVLPYFREFS 222



Query: 244 -RGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLLL 302
 N Y ++ FYV IRRRP YV++LL+PS FL+ +D + FYLP SG RV FKITLLL
 Sbjct: 223 MESSNYAEMKFYVIRRRPLFYVVSLLLPSIFLMVMDIVGFYLPNNGERSVFKITLLL 282

Query: 303 GYNVFLMMSDLLPTS--GTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR 360
 GY+VFL+++SD LP + GTPLIGVYF +C++L+V SL ETIFI L+H Q P+P
 Sbjct: 283 GYSVFLIIVSDTLPTAIGTPLIGVYFVVMALLVISLTETIFIVRLVHKQDLQ-QPVPA 341

Query: 361 WLHSLLLHCNSPGRCC-----PTAPQKENK-----GPGLTPTHLPGV----KEPEVS 403
 WL L+L + C P A + K G TH+ G K P
 Sbjct: 342 WLRHLVLERIAWLLCLREQSTSQRPPATSQATKTDDCSAMGNHCTHMGGPQDFEKS PRDR 401

Query: 404 AGQMPGPAEAELT--GGSEWTRAQREHEAQKQHSVEL---WLQFSHAMDAMLFRLLYLLFM 458
 P P EA L G + + R+ ++ E+ WL+ +D +LF +YLL +
 Sbjct: 402 CSPPPPPREASLAVCGLLQELSSIRQFLEKRDEIREVARDWLRVGSVLDKLLFHIYLLAV 461

Query: 459 ASSIITVICLWN 470
 + IT++ LW+
 Sbjct: 462 LAYSITLVMLWS 473

 >gi|30583247|qb|AAP35868.1|  5-hydroxytryptamine (serotonin) receptor 3A [Homo
 Length = 484

Score = 291 bits (744), Expect = 3e-77

Identities = 169/433 (39%), Positives = 254/433 (58%), Gaps = 33/433 (7%)

Query: 66 RKFRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPEECEGI 125
 RK RPV + PT V+I + AIL+V+E+ +L+++W W + F+ WNPE+ + I
 Sbjct: 52 RKGVRPVRDRWRKPTTVSIDVIVYAILNVDEKNQVLTYYIWRQYWTDEFLQWNPEDFDNI 111

Query: 126 TKMSMAAKNLWLPDIFIIEIEMDVKTPKGLTAYVSNEGRIRYKKPMKVDSICNLDIFYFP 185
 TK+S+ ++W+PDI I E +DV K+P Y+ ++G ++ KP++V + C+LDI+ FP
 Sbjct: 112 TKLSIPTDSIWVPDILINEFVDVGKSPNIPYVYIRHQGEVQNYKPLQVVTACSLDIYNFP 171

Query: 186 FDQQNCTLTFSFLYTVDSMLLDMEKEVWEITD---ASRNILQTHGEWELLGLSKATAKL 242
 FD QNC+LTF+S+L+T+ D+ +W + + + R++ GEWELLG+ +
 Sbjct: 172 FDVQNCSLTFTSWLHTIQ----DINISLWRLPEKVKSDRSVFMNQGEWELLGVLPYFREF 227

Query: 243 S-RGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLL 301
 S N Y ++ FYV IRRRP YV++LL+PS FL+ +D + FYLP SG RV FKITLL
 Sbjct: 228 SMESSNYAEMKFYVIRRRPLFYVVSLLLPSIFLMVMDIVGFYLPNNGERSVFKITLL 287

Query: 302 LGYNVFLMMSDLLPTS--GTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLP 359
 LGY+VFL+++SD LP + GTPLIGVYF +C++L+V SL ETIFI L+H Q P+P
 Sbjct: 288 LGYSVFLIIVSDTLPATAIGTPLIGVYFVVCMLLVISLAETIFIVRLVHKQDLQ-QPVP 346

Query: 360 RWLHSLLLHCNSPGRCC-----PTAPQKENK-----GPGLTPTHLPGV----KEPEV 402
 WL L+L + C P A + K G +H+ G K P
 Sbjct: 347 AWLRHLVLERIAWLLCLREQSTSQRPPATSQATKTDDCSAMGNHCSHMGGPQDFEKS PRD 406

Query: 403 SAGQMPGPAAEALT--GGSEWTRAQREHEAQKQHSVEL---WLQFSHAMDAMFLRLYLLF 457
 P P EA L G + + R+ ++ E+ WL+ +D +LF +YLL
 Sbjct: 407 RCSPPPPPREASLAVCGLLQELSSIRQFLEKRDEIREVARDWLRVGSVLDKLLFHIYLLA 466

Query: 458 MASSIITVICLWN 470
 + + IT++ LW+
 Sbjct: 467 VLAYSITLVMLWS 479

┐>gi|4504543|ref|NP_000860.1| **L** 5-hydroxytryptamine (serotonin) receptor 3A; 5-HT
 5-hydroxytryptamine (serotonin) receptor-3 [Homo
 sapiens]

gi|1168222|sp|P46098|5HT3_HUMAN **L** 5-hydroxytryptamine 3 receptor precursor (5-HT-
 ion channel receptor) (5-HT3R)

gi|681914|dbj|BAA08387.1| **L** serotonin 5-HT3 receptor [Homo sapiens]

gi|3115224|emb|CAA05852.1| **L** 5-hydroxytryptamine3 receptor [Homo sapiens]

gi|9715820|emb|CAA06442.3| serotonin 3 receptor [Homo sapiens]

gi|12803101|gb|AAH02354.1| **L** 5-hydroxytryptamine (serotonin) receptor 3A [Homo sa]

gi|20379142|gb|AAM21131.1| **L** 5-hydroxytryptamine receptor 3A [Homo sapiens]

gi|37514834|gb|AAH04453.2| **L** 5-hydroxytryptamine (serotonin) receptor 3A [Homo sa]
 Length = 478

Score = 291 bits (744), Expect = 3e-77

Identities = 169/433 (39%), Positives = 254/433 (58%), Gaps = 33/433 (7%)

Query: 66 RKPFRPVTNISVPTQVNISFAMSAILDVNEQLHLSSFLWLEMVWDNPFISWNPEECEGI 125
 RK RPV + PT V+I + AIL+V+E+ +L+++W W + F+ WNPE+ + I
 Sbjct: 46 RKGVRPVRDWRKPPTTVSIDVIVYAILNVDEKNQVLTYYIWRQYWTDEFLQWNPEDFDNI 105

Query: 126 TKMSMAAKNLWLPDIFIIEIEMDVKTPKGLTAYVSNEGRIRYKKPMKVDSICNLDIYFYP 185
 TK+S+ ++W+PDI I E +DV K+P Y+ ++G ++ KP++V + C+LDI+ FP
 Sbjct: 106 TKLSIPTDSIWVPDILINEFVDVGKSPNIPYVYIRHQGEVQNYKPLQVVTACSLDIYNFP 165

Query: 186 FDQQNCTLTFSSFLYTVDMSLLDMEKEVWEITD---ASRNILQTHGEWELLGLSKATAKL 242
 FD QNC+LTF+S+L+T+ D+ +W + + + R++ GEWELLG+ +
 Sbjct: 166 FDVQNCSTLFTSWLHTIQ----DINISLWRLPEKVKSDRSVFMNQGEWELLGVLPYFREF 221

Query: 243 S-RGGNLYDQIVFYVAIRRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLL 301
 S N Y ++ FYV IRRRP YV++LL+PS FL+ +D + FYLP SG RV FKITLL
 Sbjct: 222 SMESSNYAEMKFYVIRRRRPLFYVVSLLLPSIFLMVMDIVGFYLPNSGERVSFKITLL 281

Query: 302 LGYNVFLMMSDLLPTS--GTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLP 359
 LGY+VFL+++SD LP + GTPLIGVYF +C++L+V SL ETIFI L+H Q P+P
 Sbjct: 282 LGYSVFLIIVSDTLPATAIGTPLIGVYFVVCMLLVISLAETIFIVRLVHKQDLQ-QPVP 340

Query: 360 RWLHSLLLHCNSPGRCC-----PTAPQKENK-----GPGLTPTHLPGV----KEPEV 402
 WL L+L + C P A + K G +H+ G K P
 Sbjct: 341 AWLRHLVLERIAWLLCLREQSTSQRPPATSQATKTDDCSAMGNHCSHMGGPQDFEKS PRD 400

Query: 403 SAGQMPGPAAELT--GGSEWTRAQREHEAQKQHSVEL---WLQFSHAMDAMLFRLYLLF 457
 P P E A L G + + R+ ++ E+ WL+ +D +LF +YLL
 Sbjct: 401 RCSPPPPPREASLAVCGLLQELSSIRQFLEKRDEIREVARDWLRVGSVLDKLLFHIYLLA 460

Query: 458 MASSIITVICLWN 470
 + + IT++ LW+
 Sbjct: 461 VLAYSITLVMLWS 473

└─>gi|30585371|gb|AAP36958.1| Homo sapiens 5-hydroxytryptamine (serotonin) recept
 construct]
 Length = 485

Score = 291 bits (744), Expect = 3e-77
 Identities = 169/433 (39%), Positives = 254/433 (58%), Gaps = 33/433 (7%)

Query: 66 RKPFRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPEECEGI 125
 RK RPV + PT V+I + AIL+V+E+ +L++++W W + F+ WNPE+ + I
 Sbjct: 52 RKGVRPVRDWRKPTTVSIDVIVYAILNVDEKNQVLTYYIWYRQYWTDEFLQWNPEDFDNI 111

Query: 126 TKMSMAAKNLWLPDIFIIEIEMDVKTPKGLTAYVSNRIRYKKPMKVDSICNLDIFYFP 185
 TK+S+ ++W+PDI I E +DV K+P Y+ ++G ++ KP++V + C+LDI+ FP
 Sbjct: 112 TKLSIPTDSIWWPDILINEFVDVGKSPNIPYVYIRHQGEVQNYKPLQVVTACSLDIYNFP 171

Query: 186 FDQQNCTLTFSSFLYTVDSMLLDMEKEVWEITD---ASRNILQTHGEWELLGLSKATAKL 242
 FD QNC+LTF+S+L+T+ D+ +W + + + R++ GEWELLG+ +
 Sbjct: 172 FDVQNCSLTFTSWLHTIQ----DINISLWRLPEKVKSDRSVFMNQGEWELLGVLPYFREF 227

Query: 243 S-RGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLL 301
 S N Y ++ FYV IRRRP YV++LL+PS FL+ +D + FYLP SG RV FKITLL
 Sbjct: 228 SMESSNYAEMKFYVIRRRPLFYVVSLLLPSIFLMVMDIVGFYLPNPSGERVSFKITLL 287

Query: 302 LGYNVFLLMMSDLLPTS--GTPLIGVYFALCLSLMVGSLETFIFITHLLHVATTQPPPLP 359
 LGY+VFL+++SD LP + GTPLIGVYF +C++L+V SL ETIFI L+H Q P+P
 Sbjct: 288 LGYSVFLIIVSDTLPTAIGTPLIGVYFVVMALLVISLAETIFIVRLVHKQDLQ-QPVP 346

Query: 360 RWLHSLLLHCNSPGRCC-----PTAPQKENK-----GPGLTPTHLPGV-----KEPEV 402
 WL L+L + C P A + K G +H+ G K P
 Sbjct: 347 AWLRHLVLERIAWLLCLREQSTSQRPPATSQATKTDDCSAMGNHCSHMGPPQDFEKSPRD 406

Query: 403 SAGQMPGPAAELT--GGSEWTRAQREHEAQKQHSVEL---WLQFSHAMDAMLFRLYLLF 457
 P P E A L G + + R+ ++ E+ WL+ +D +LF +YLL
 Sbjct: 407 RCSPPPPPREASLAVCGLLQELSSIRQFLEKRDEIREVARDWLRVGSVLDKLLFHIYLLA 466

Query: 458 MASSIITVICLWN 470
 + + IT++ LW+
 Sbjct: 467 VLAYSITLVMLWS 479

└─>gi|1586341|prf||2203408A serotonin 3AS receptor
 Length = 478

Score = 290 bits (742), Expect = 5e-77
 Identities = 169/432 (39%), Positives = 253/432 (58%), Gaps = 33/432 (7%)

Query: 67 KPFPRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPEECEGIT 126
 K RPV + PT V+I + AIL+V+E+ +L++++W W + F+ WNPE+ + IT

Sbjct: 47 KGVPRVDRWRKPTTVSIDVIVYAILNVDEKNQVLTTYIWYRQYWTDEFLQWNPEDFDNIT 106

Query: 127 KMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLDIFYFPF 186
K+S+ ++W+PDI I E +DV K+P Y+ ++G ++ KP++V + C+LDI+ FPF

Sbjct: 107 KLSIPTDSIWVPDILINEFVDVGKSPNIPYVYIRHQGEVQNYKPLQVVTACSLDIYNFPF 166

Query: 187 DQQNCTLTFFSFLYTVDSMLLDMEKEVWEITD---ASRNILQTHGEWELLGLSKATAKLS 243
D QNC+LTF+S+L+T+ D+ +W + + + R++ GEWELLG+ + S

Sbjct: 167 DVQNCSLTFTSWLHTIQ---DINISLWRLPEKVKSDRSVFMNQGEWELLGVLPHYFREFFS 222

Query: 244 -RGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLLL 302
N Y ++ FYV IRRRP YV++LL+PS FL+ +D + FYLP SG RV FKITLLL

Sbjct: 223 MESSNYAEMKFYVIRRRPLFYVVSLLLPSIFLMVMDIVGFYLPNSGERVSFKITLLL 282

Query: 303 GYNVFLMMSDLLPTS--GTPLIGVYFALCLSLMVGSLLLETIFITHLLHVATTQPPPLPR 360
GY+VFL+++SD LP + GTPLIGVYF +C++L+V SL ETIFI L+H Q P+P

Sbjct: 283 GYSVFLIIVSDTLPTATAIGTPLIGVYFVVCMAALLVISLTETIFIVRLVHKQDLQ-QPVPA 341

Query: 361 WLHSLLLHCNSPGRCC-----PTAPQKENK-----GPGLTPTHLPGV----KEPEVS 403
WL L+L + C P A + K G TH+ G K P

Sbjct: 342 WLRHLVLERIAWLLCLREQSTSQRPPATSQATKTDDCSAMGNHCTHMGGPQDFEKS PRDR 401

Query: 404 AGQMPGPAEAEILT--GGSEWTRAQREHEAQKQHSVEL---WLQFSHAMDAMLFRLYLLFM 458
P P EA L G + + R+ ++ E+ WL+ +D +LF +YLL +

Sbjct: 402 CSPPPPPREASLAVCGLLQELSSIRQFLEKRDEIREVARDWLRVGSVLDKLLFHIYLLAV 461

Query: 459 ASSIITVICLWN 470
+ IT++ LW+

Sbjct: 462 LAYSITLVMLWS 473

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Dec 29, 2003 2:09 AM
Number of letters in database: 519,349,222
Number of sequences in database: 1,585,607

Lambda	K	H
0.323	0.138	0.429

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 50,992,532
Number of Sequences: 1585607
Number of extensions: 2252786
Number of successful extensions: 5073
Number of sequences better than 10.0: 97
Number of HSP's better than 10.0 without gapping: 76
Number of HSP's successfully gapped in prelim test: 21

Number of HSP's that attempted gapping in prelim test: 4817
 Number of HSP's gapped (non-prelim): 103
 length of query: 471
 length of database: 519,349,222
 effective HSP length: 128
 effective length of query: 343
 effective length of database: 316,391,526
 effective search space: 108522293418
 effective search space used: 108522293418
 T: 11
 A: 40
 X1: 16 (7.5 bits)
 X2: 38 (14.6 bits)
 X3: 64 (24.7 bits)
 S1: 41 (22.0 bits)
 S2: 75 (33.5 bits)